SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT:
        (A) NAME: Forschungszentrum Juelich GmbH
        (B) ADDRESS: Postfach 1913
        (C) CITY: Juelich
        (E) COUNTRY: GERMANY
        (F) ZIP CODE: 52425

    (ii) TITLE OF INVENTION: METHOD FOR MICROBIAL PRODUCTION OF AMINO ACIDS
                           OF THE ASPARTATE AND/OR GLUTAMATE FAMILY

    (iii) NUMBER OF SEQUENCES: 2

    (iv) COMPUTER-READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3728 Base Pairs
        (B) Type: Nucleotide
        (C) Strandedness: Single strand
        (D) TOPOLOGY: linear

    (ii) TYPE OF MOLECULE: Genomic DNA

    (xi) SEQ ID NO: 1:

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CGCAACCGTG CTTGAAGTCG TGCAGGTCAG GGGAGTGTTG CCCGAAAACA TTGAGAGGAA        60

AACAAAAACC GATGTTTGAT TGGGGGAATC GGGGGTTACG ATACTAGGAC GCAGTGACTG       120

CTATCACCCT TGGCGGTCTC TTGTTGAAAG GAATAATTAC TCTAGTGTCG ACTCACACAT       180

CTTCAACGCT TCCAGCATTC AAAAAGATCT TGGTAGCAAA CCGCGGCGAA ATCGCGGTCC       240

GTGCTTTCCG TGCAGCACTC GAAACCGGTG CAGCCACGGT AGCTATTTAC CCCCGTGAAG       300

ATCGGGGATC ATTCCACCGC TCTTTTGCTT CTGAAGCTGT CCGCATTGGT ACCGAAGGCT       360

CACCAGTCAA GGCGTACCTG GACATCGATG AAATTATCGG TGCAGCTAAA AAAGTTAAAG       420

CAGATGCCAT TTACCCGGGA TACGGCTTCC TGTCTGAAAA TGCCCAGCTT GCCCGCGAGT       480
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GTGCGGAAAA CGGCATTACT TTTATTGGCC CAACCCCAGA GGTTCTTGAT CTCACCGGTG    540

ATAAGTCTCG CGCGGTAACC GCCGCGAAGA AGGCTGGTCT GCCAGTTTTG GCGGAATCCA    600

CCCCGAGCAA AAACATCGAT GAGATCGTTA AAAGCGCTGA AGGCCAGACT TACCCCATCT    660

TTGTGAAGGC AGTTGCCGGT GGTGGCGGAC GCGGTATGCG TTTTGTTGCT TCACCTGATG    720

AGCTTCGCAA ATTAGCAACA GAAGCATCTC GTGAAGCTGA AGCGGCTTTC GGCGATGGCG    780

CGGTATATGT CGAACGTGCT GTGATTAACC CTCAGCATAT TGAAGTGCAG ATCCTTGGCG    840

ATCACACTGG AGAAGTTGTA CACCTTTATG AACGTGACTG CTCACTGCAG CGTCGTCACC    900

AAAAAGTTGT CGAAATTGCG CCAGCACAGC ATTTGGATCC AGAACTGCGT GATCGCATTT    960

GTGCGGATGC AGTAAAGTTC TGCCGCTCCA TTGGTTACCA GGGCGCGGGA ACCGTGGAAT   1020

TCTTGGTCGA TGAAAGGGC AACCACGTCT TCATCGAAAT GAACCCACGT ATCCAGGTTG   1080

AGCACACCGT GACTGAAGAA GTCACCGAGG TGGACCTGGT GAAGGCGCAG ATGCGCTTGG   1140

CTGCTGGTGC AACCTTGAAG GAATTGGGTC TGACCCAAGA TAAGATCAAG ACCCACGGTG   1200

CAGCACTGCA GTGCCGCATC ACCACGGAAG ATCCAAACAA CGGCTTCCGC CCAGATACCG   1260

GAACTATCAC CGCGTACCGC TCACCAGGCG GAGCTGGCGT TCGTCTTGAC GGTGCAGCTC   1320

AGCTCGGTGG CGAAATCACC GCACACTTTG ACTCCATGCT GGTGAAAATG ACCTGCCGTG   1380

GTTCCGACTT TGAAACTGCT GTTGCTCGTG CACAGCGCGC GTTGGCTGAG TTCACCGTGT   1440

CTGGTGTTGC AACCAACATT GGTTTCTTGC GTGCGTTGCT GCGGGAAGAG GACTTCACTT   1500

CCAAGCGCAT CGCCACCGGA TTCATTGCCG ATCACCCGCA CCTCCTTCAG GCTCCACCTG   1560

CTGATGATGA GCAGGGACGC ATCCTGGATT ACTTGGCAGA TGTCACCGTG AACAAGCCTC   1620

ATGGTGTGCG TCCAAAGGAT GTTGCAGCTC CTATCGATAA GCTGCCTAAC ATCAAGGATC   1680

TGCCACTGCC ACGCGGTTCC CGTGACCGCC TGAAGCAGCT TGGCCCAGCC GCGTTTGCTC   1740

GTGATCTCCG TGAGCAGGAC GCACTGGCAG TTACTGATAC CACCTTCCGC GATGCACACC   1800

AGTCTTTGCT TGCGACCCGA GTCCGCTCAT TCGCACTGAA GCCTGCGGCA GAGGCCGTCG   1860

CAAAGCTGAC TCCTGAGCTT TTGTCCGTGG AGGCCTGGGG CGGCGCGACC TACGATGTGG   1920

CGATGCGTTT CCTCTTTGAG GATCCGTGGG ACAGGCTCGA CGAGCTGCGC GAGGCGATGC   1980

CGAATGTAAA CATTCAGATG CTGCTTCGCG CCGCAACAC CGTGGGATAC ACCCCGTACC    2040

CAGACTCCGT CTGCCGCGCG TTTGTTAAGG AAGCTGCCAG CTCCGGCGTG GACATCTTCC   2100
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GCATCTTCGA CGCGCTTAAC GACGTCTCCC AGATGCGTCC AGCAATCGAC GCAGTCCTGG    2160

AGACCAACAC CGCGGTAGCC GAGGTGGCTA TGGCTTATTC TGGTGATCTC TCTGATCCAA    2220

ATGAAAAGCT CTACACCCTG GATTACTACC TAAAGATGGC AGAGGAGATC GTCAAGTCTG    2280

GCGCTCACAT CTTGGCCATT AAGGATATGG CTGGTCTGCT TCGCCCAGCT GCGGTAACCA    2340

AGCTGGTCAC CGCACTGCGC CGTGAATTCG ATCTGCCAGT GCACGTGCAC ACCCACGACA    2400

CTGCGGGTGG CCAGCTGGCA ACCTACTTTG CTGCAGCTCA AGCTGGTGCA GATGCTGTTG    2460

ACGGTGCTTC CGCACCACTG TCTGGCACCA CCTCCCAGCC ATCCCTGTCT GCCATTGTTG    2520

CTGCATTCGC GCACACCCGT CGCGATACCG GTTTGAGCCT CGAGGCTGTT TCTGACCTCG    2580

AGCCGTACTG GGAAGCAGTG CGCGGACTGT ACCTGCCATT TGAGTCTGGA ACCCCAGGCC    2640

CAACCGGTCG CGTCTACCGC CACGAAATCC CAGGCGGACA GTTGTCCAAC CTGCGTGCAC    2700

AGGCCACCGC ACTGGGCCTT GCGGATCGTT TCGAACTCAT CGAAGACAAC TACGCAGCCG    2760

TTAATGAGAT GCTGGGACGC CCAACCAAGG TGACCCCATC CTCCAAGGTT GTTGGCGACC    2820

TCGCACTCCA CCTCGTTGGT GCGGGTGTGG ATCCAGCAGA CTTTGCTGCC GATCCACAAA    2880

AGTACGACAT CCCAGACTCT GTCATCGCGT TCCTGCGCGG CGAGCTTGGT AACCCTCCAG    2940

GTGGCTGGCC AGAGCCACTG CGCACCCGCG CACTGGAAGG CCGCTCCGAA GGCAAGGCAC    3000

CTCTGACGGA AGTTCCTGAG GAAGAGCAGG CGCACCTCGA CGCTGATGAT TCCAAGGAAC    3060

GTCGCAATAG CCTCAACCGC CTGCTGTTCC CGAAGCCAAC CGAAGAGTTC CTCGAGCACC    3120

GTCGCCGCTT CGGCAACACC TCTGCGCTGG ATGATCGTGA ATTCTTCTAC GGCCTGGTCG    3180

AAGGCCGCGA GACTTTGATC CGCCTGCCAG ATGTGCGCAC CCCACTGCTT GTTCGCCTGG    3240

ATGCGATCTC TGAGCCAGAC GATAAGGGTA TGCGCAATGT TGTGGCCAAC GTCAACGGCC    3300

AGATCCGCCC AATGCGTGTG CGTGACCGCT CCGTTGAGTC TGTCACCGCA ACCGCAGAAA    3360

AGGCAGATTC CTCCAACAAG GGCCATGTTG CTGCACCATT CGCTGGTGTT GTCACCGTGA    3420

CTGTTGCTGA AGGTGATGAG GTCAAGGCTG AGATGCAGT CGCAATCATC GAGGCTATGA    3480

AGATGGAAGC AACAATCACT GCTTCTGTTG ACGGCAAAAT CGATCGCGTT GTGGTTCCTG    3540

CTGCAACGAA GGTGGAAGGT GGCGACTTGA TCGTCGTCGT TTCCTAAACC TTTCTGTAAA    3600

AAGCCCCGCG TCTTCCTCAT GGAGGAGGCG GGGCTTTTTG GGCCAAGATG GGAGATGGGT    3660

GAGTTGGATT TGGTCTGATT CGACACTTTT AAGGGCAGAG ATTTGAAGAT GGAGACCAAG    3720
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GCTCAAAG

(2) SEQ ID NO: 2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1140 Amino Acids
        (B) TYPE: Amino Acid
        (C) STRANDEDNESS: Single Strand
        (D) TOPOLOGY: linear

    (ii)TYPE OF MOLECULE: Protein

    (xi) SEQ ID NO: 2:

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Met Ser Thr His Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile Leu
1               5                   10                  15

Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Leu
            20                  25                  30

Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly
            35                  40                  45

Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu
50                  55                      60

Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala
65                  70                  75                      80

Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu
                85                  90                  95

Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr
            100                 105                 110

Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser
            115                 120                 125

Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu
        130                 135                 140

Ser Thr Pro Ser Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu Gly
145                 150                 155                 160

Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg
                165                 170                 175

Gly Met Arg Phe Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr
            180                 185                 190

Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr
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        195                    200                    205

Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile Leu
    210                     215                 220

Gly Asp His Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys Ser
225                 230                 235                     240

Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His
                245                 250                     255

Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe
            260                 265                 270

Cys Arg Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val
        275                 280                 285

Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln
    290                 295                 300

Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val Lys
305                 310                 315                     320

Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu
                325                 330                     335

Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg Ile
                340                 345                 350

Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile
        355                 360                 365

Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala
    370                 375                 380

Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val
385                 390                 395                     400

Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg Ala
            405                 410                     415

Gln Arg Ala Leu Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn Ile
        420                 425                     430

Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg
        435                 440                 445

Ile Ala Thr Gly Phe Ile Ala Asp His Pro His Leu Leu Gln Ala Pro
    450                 455                 460

Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val
465                 470                 475                     480

Thr Val Asn Lys Pro His Gly Val Arg Pro Lys Asp Val Ala Ala Pro
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                485                    490                    495
Ile Asp Lys Leu Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser
        500                    505                    510

Arg Asp Arg Leu Lys Gln Leu Gly Pro Ala Ala Phe Ala Arg Asp Leu
        515                    520                    525

Arg Glu Gln Asp Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala
    530                    535                    540

His Gln Ser Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro
545                    550                    555                    560

Ala Ala Glu Ala Val Ala Lys Lys Thr Pro Glu Leu Leu Ser Val Glu
                565                    570                    575

Ala Trp Gly Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu
                580                    585                    590

Asp Pro Trp Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val
        595                    600                    605

Asn Ile Gln Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro
    610                    615                    620

Tyr Pro Asp Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser
625                    630                    635                    640

Gly Val Asp Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln
                645                    650                    655

Met Arg Pro Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala
                660                    665                    670

Glu Val Ala Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys
        675                    680                    685

Leu Tyr Thr Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys
        690                    695                    700

Ser Gly Ala His Ile Leu Ala Ile Lys Asp Met Xaa Gly Leu Leu Arg
705                    710                    715                    720

Pro Ala Ala Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp
                725                    730                    735

Leu Pro Val His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala
                740                    745                    750

Thr Tyr Phe Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala
        755                    760                    765

Ser Ala Pro Leu Ser Gly Thr Thr Ser Gln Pro Ser Leu Ser Ala Ile
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                770              775                 780

Val Ala Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu
785              790              795                 800

Ala Val Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr
             805              810              815

Leu Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg
             820              825              830

His Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr
         835              840              845

Ala Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala
    850              855              860

Ala Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser
865              870              875                 880

Lys Val Val Gly Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp
             885              890              895

Pro Ala Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser
             900              905              910

Val Ile Ala Phe Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp
         915              920              925

Pro Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys
    930              935              940

Ala Pro Leu Thr Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala
945              950              955                 960

Asp Asp Ser Lys Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro
             965              970              975

Lys Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr
             980              985              990

Ser Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg
    995              1000             1005

Glu Thr Leu Ile Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg
    1010             1015             1020

Leu Asp Ala Ile Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val
1025             1030             1035             1040

Ala Asn Val Asn Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser
             1045             1050             1055

Val Glu Ser Val Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys
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        1060                 1065                     1070

Gly His Val Ala Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala
        1075              1080              1085

Glu Gly Asp Glu Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala
        1090              1095              1100

Met Lys Met Glu Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp
1105              1110              1115              1120

Arg Val Val Val Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile
              1125              1130              1135

Val Val Val Ser
        1140
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